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Sequence Listing could not be accepted.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: [year=2007; month=12; day=13; hr=14; min=24; sec=41; ms=226;
]

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Reviewer Comments:

Seq Id 19 through 23

Invalid response for <213>, It can be either Artificial, Unknown or
Genus species.

Please check for the similar errors in subsequent sequences.

Application No: 10511384

Version No: 2.0

Input Set:**Output Set:****Started:** 2007-11-28 14:28:36.627**Finished:** 2007-11-28 14:28:41.238**Elapsed:** 0 hr(s) 0 min(s) 4 sec(s) 611 ms**Total Warnings:** 229**Total Errors:** 0**No. of SeqIDs Defined:** 229**Actual SeqID Count:** 229

| Error code | Error Description |
|------------|---|
| W 213 | Artificial or Unknown found in <213> in SEQ ID (1) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (2) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (3) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (4) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (5) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (6) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (7) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (8) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (9) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (10) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (11) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (12) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (13) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (14) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (15) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (16) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (17) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (18) |
| W 402 | Undefined organism found in <213> in SEQ ID (19) |
| W 402 | Undefined organism found in <213> in SEQ ID (20) |

Input Set:

Output Set:

Started: 2007-11-28 14:28:36.627

Finished: 2007-11-28 14:28:41.238

Elapsed: 0 hr(s) 0 min(s) 4 sec(s) 611 ms

Total Warnings: 229

Total Errors: 0

No. of SeqIDs Defined: 229

Actual SeqID Count: 229

| Error code | Error Description |
|------------|--|
| W 402 | Undefined organism found in <213> in SEQ ID (21) |
| W 402 | Undefined organism found in <213> in SEQ ID (22) |
| W 402 | Undefined organism found in <213> in SEQ ID (23) |
| W 402 | Undefined organism found in <213> in SEQ ID (24) |
| W 402 | Undefined organism found in <213> in SEQ ID (25) |
| W 402 | Undefined organism found in <213> in SEQ ID (26) |
| W 402 | Undefined organism found in <213> in SEQ ID (27) |
| W 402 | Undefined organism found in <213> in SEQ ID (28) |
| W 402 | Undefined organism found in <213> in SEQ ID (29) |
| W 402 | Undefined organism found in <213> in SEQ ID (30) |
| W 402 | Undefined organism found in <213> in SEQ ID (31) |
| W 402 | Undefined organism found in <213> in SEQ ID (32) |
| W 402 | Undefined organism found in <213> in SEQ ID (33) |
| W 402 | Undefined organism found in <213> in SEQ ID (34) |
| W 402 | Undefined organism found in <213> in SEQ ID (35) |
| W 402 | Undefined organism found in <213> in SEQ ID (36) |
| W 402 | Undefined organism found in <213> in SEQ ID (37) |
| W 402 | Undefined organism found in <213> in SEQ ID (38) |

This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

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<120> Antiangiogenic active immunotherapies

<130> 976-19 PCT/US

<140> 10511384

<141> 2007-11-28

<150> CU 2002/0076

<151> 2002-04-15

<150> EP98001000

<151> 1998-01-31

<160> 229

<170> PatentIn version 3.4

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<213> Artificial Sequence

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<213> Artificial Sequence

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<223> primer

<400> 3

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<213> Artificial Sequence

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<220>
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<210> 7
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<212> DNA
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<400> 7
tggatccatg aactttctgc t 21

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<400> 13
 gaagatctgt ataaggactt c 21

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<220>
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<400> 16
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<220>
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<400> 18
tagcggccgc ttaaacagg

19

<210> 19
<211> 408
<212> PRT
<213> VEGF121 Isoform

<400> 19

Met Glu Thr Ala Ser Asn Pro His Glu Leu Glu Leu Glu Ser Glu Arg
1 5 10 15

Thr Arg Pro Val Ala Leu His Ile Ser Thr Arg Pro Ser Glu Arg Leu
20 25 30

Glu Ala Leu Ala Leu Glu Leu Glu Leu Glu Thr Tyr Arg Leu Glu His
35 40 45

Ile Ser His Ile Ser Ala Leu Ala Leu Tyr Ser Thr Arg Pro Ser Glu
50 55 60

Arg Gly Leu Asn Ala Leu Ala Ala Leu Ala Pro Arg Met Glu Thr Ala
65 70 75 80

Leu Ala Gly Leu Gly Leu Tyr Gly Leu Tyr Gly Leu Tyr Gly Leu Asn
85 90 95

Ala Ser Asn His Ile Ser His Ile Ser Gly Leu Val Ala Leu Val Ala
100 105 110

Leu Leu Tyr Ser Pro His Glu Met Glu Thr Ala Ser Pro Val Ala Leu
115 120 125

Thr Tyr Arg Gly Leu Asn Ala Arg Gly Ser Glu Arg Thr Tyr Arg Cys
130 135 140

Tyr Ser His Ile Ser Pro Arg Ile Leu Glu Gly Leu Thr His Arg Leu
145 150 155 160

Glu Val Ala Leu Ala Ser Pro Ile Leu Glu Pro His Glu Gly Leu Asn
165 170 175

Gly Leu Thr Tyr Arg Pro Arg Ala Ser Pro Gly Leu Ile Leu Glu Gly
180 185 190

Leu Thr Tyr Arg Ile Leu Glu Pro His Glu Leu Tyr Ser Pro Arg Ser
195 200 205

Glu Arg Cys Tyr Ser Val Ala Leu Pro Arg Leu Glu Met Glu Thr Ala
210 215 220

Arg Gly Cys Tyr Ser Gly Leu Tyr Gly Leu Tyr Cys Tyr Ser Cys Tyr
225 230 235 240

Ser Ala Ser Asn Ala Ser Pro Gly Leu Gly Leu Tyr Leu Glu Gly Leu
245 250 255

Cys Tyr Ser Val Ala Leu Pro Arg Thr His Arg Gly Leu Gly Leu Ser
260 265 270

Glu Arg Ala Ser Asn Ile Leu Glu Thr His Arg Met Glu Thr Gly Leu
275 280 285

Asn Ile Leu Glu Met Glu Thr Ala Arg Gly Ile Leu Glu Leu Tyr Ser
290 295 300

Pro Arg His Ile Ser Gly Leu Asn Gly Leu Tyr Gly Leu Asn His Ile
305 310 315 320

Ser Ile Leu Glu Gly Leu Tyr Gly Leu Met Glu Thr Ser Glu Arg Pro
325 330 335

His Glu Leu Glu Gly Leu Asn His Ile Ser Ala Ser Asn Leu Tyr Ser
340 345 350

Cys Tyr Ser Gly Leu Cys Tyr Ser Ala Arg Gly Pro Arg Leu Tyr Ser
355 360 365

Leu Tyr Ser Ala Ser Pro Ala Arg Gly Ala Leu Ala Ala Arg Gly Gly
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Leu Asn Gly Leu Leu Tyr Ser Cys Tyr Ser Ala Ser Pro Leu Tyr Ser

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Pro Arg Ala Arg Gly Ala Arg Gly
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<210> 20

<211> 444

<212> DNA

<213> VEGF121 Isoform

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gtgaagttca tggatgtcta tcagcgcagc tactgccatc caatcgagac cctggtggac    180
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atgcgatgcg ggggctgctg caatgacgag ggcttgaggt gtgtgcccac tgaggagtcc    300
aacatcacca tgcagattat gcggatcaaa cctcaccaag gccagcacat aggagagatg    360
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aatgtgaca agccgaggcg gtga                                           444
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<210> 21

<211> 408

<212> PRT

<213> VEGF mutated isoform

<400> 21

Met Glu Thr Ala Ser Asn Pro His Glu Leu Glu Leu Glu Ser Glu Arg
1 5 10 15

Thr Arg Pro Val Ala Leu His Ile Ser Thr Arg Pro Ser Glu Arg Leu
20 25 30

Glu Ala Leu Ala Leu Glu Leu Glu Leu Glu Thr Tyr Arg Leu Glu His
35 40 45

Ile Ser His Ile Ser Ala Leu Ala Leu Tyr Ser Thr Arg Pro Ser Glu
50 55 60

Arg Gly Leu Asn Ala Leu Ala Ala Leu Ala Pro Arg Met Glu Thr Ala
65 70 75 80

Leu Ala Gly Leu Gly Leu Tyr Gly Leu Tyr Gly Leu Tyr Gly Leu Asn
85 90 95

Ala Ser Asn His Ile Ser His Ile Ser Gly Leu Val Ala Leu Val Ala
100 105 110

Leu Leu Tyr Ser Pro His Glu Met Glu Thr Ala Ser Pro Val Ala Leu
115 120 125

Thr Tyr Arg Gly Leu Asn Ala Arg Gly Ser Glu Arg Thr Tyr Arg Cys
130 135 140

Tyr Ser His Ile Ser Pro Arg Ile Leu Glu Gly Leu Thr His Arg Leu
145 150 155 160

Glu Val Ala Leu Ala Ser Pro Ile Leu Glu Pro His Glu Gly Leu Asn
165 170 175

Gly Leu Thr Tyr Arg Pro Arg Ala Ser Pro Gly Leu Ile Leu Glu Gly
180 185 190

Leu Thr Tyr Arg Ile Leu Glu Pro His Glu Leu Tyr Ser Pro Arg Ser
195 200 205

Glu Arg Cys Tyr Ser Val Ala Leu Pro Arg Leu Glu Met Glu Thr Ala
210 215 220

Arg Gly Cys Tyr Ser Gly Leu Tyr Gly Leu Tyr Cys Tyr Ser Cys Tyr
225 230 235 240

Ser Ala Ser Asn Ala Ser Pro Gly Leu Gly Leu Tyr Leu Glu Gly Leu
245 250 255

Cys Tyr Ser Val Ala Leu Pro Arg Thr His Arg Gly Leu Gly Leu Ser
260 265 270

Glu Arg Ala Ser Asn Ile Leu Glu Thr His Arg Met Glu Thr Gly Leu
275 280 285

Asn Ile Leu Glu Met Glu Thr Ala Leu Ala Ile Leu Glu Ala Leu Ala
290 300

Pro Arg Ala Leu Ala Gly Leu Asn Gly Leu Tyr Gly Leu Asn His Ile

305 310 315 320

Ser Ile Leu Glu Gly Leu Tyr Gly Leu Met Glu Thr Ser Glu Arg Pro
325 330 335

His Glu Leu Glu Gly Leu Asn His Ile Ser Ala Ser Asn Leu Tyr Ser
340 345 350

Cys Tyr Ser Gly Leu Cys Tyr Ser Ala Arg Gly Pro Arg Leu Tyr Ser
355 360 365

Leu Tyr Ser Ala Ser Pro Ala Arg Gly Ala Leu Ala Ala Arg Gly Gly
370 375 380

Leu Asn Gly Leu Leu Tyr Ser Cys Tyr Ser Ala Ser Pro Leu Tyr Ser
385 390 395 400

Pro Arg Ala Arg Gly Ala Arg Gly
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<210> 22
<211> 444
<212> DNA
<213> VEGF mutated isoform

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gtgaagttca tggatgtcta tcagcgcagc tactgccatc caatcgagac cctggtggac 180
atcttccagg agtaccctga tgagatcgag tacatcttca agccatcctg tgtgcccctg 240
atgcatgacg ggggctgctg caatgacgag ggcctggagt gtgtgcccac tgaggagtcc 300
aacatcacca tgcagattat ggcaatcgca cctgcacaag gccagcacat aggagagatg 360
agcttcctac agcacaacaa atgtgaatgc agaccaaaga aagatagagc aagacaagaa 420
aatgtgaca agccgaggcg gtaa 444

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<211> 887
<212> PRT
<213> KDR 1-3 fragments

<400> 23

Met Glu Thr Gly Leu Ser Glu Arg Leu Tyr Ser Val Ala Leu Leu Glu
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Leu Glu Ala Leu Ala Val Ala Leu Ala Leu Ala Leu Glu Thr Arg Pro
20 25 30

Leu Glu Cys Tyr Ser Val Ala Leu Gly Leu Thr His Arg Ala Arg Gly
35 40 45

Ala Leu Ala Ala Leu Ala Ser Glu Arg Val Ala Leu Gly Leu Tyr Leu
50 55 60

Glu Pro Arg Ser Glu Arg Val Ala Leu Ser Glu Arg Leu Glu Ala Ser
65 70 75 80

Pro Leu Glu Pro Arg Ala Arg Gly Leu Glu Ser Glu Arg Ile Leu Glu
85 90 95

Gly Leu Asn Leu Tyr Ser Ala Ser Pro Ile Leu Glu Leu Glu Thr His
100 105 110

Arg Ile Leu Glu Leu Tyr Ser Ala Leu Ala Ala Ser Asn Thr His Arg
115 120 125

Thr His Arg Leu Glu Gly Leu Asn Ile Leu Glu Thr His Arg Cys Tyr
130 135 140

Ser Ala Arg Gly Gly Leu Tyr Gly Leu Asn Ala Arg Gly Ala Ser Pro
145 150 155 160

Leu Glu Ala Ser Pro Thr Arg Pro Leu Glu Thr Arg Pro Pro Arg Ala
165 170 175

Ser Asn Ala Ser Asn Gly Leu Asn Ser Glu Arg Gly Leu Tyr Ser Glu
180 185 190

Arg Gly Leu Gly Leu Asn Ala Arg Gly Val Ala Leu Gly Leu Val Ala
195 200 205

Leu Thr His Arg Gly Leu Cys Tyr Ser Ser Glu Arg Ala Ser Pro Gly
210 215 220

Leu Tyr Leu Glu Pro His Glu Cys Tyr Ser Leu Tyr Ser Thr His Arg

| | | | |
|---|-----|-----|-----|
| 225 | 230 | 235 | 240 |
| Leu Glu Thr His Arg Ile Leu Glu Pro Arg Leu Tyr Ser Val Ala Leu | | | |
| 245 | 250 | 255 | |
| Ile Leu Glu Gly Leu Tyr Ala Ser Asn Ala Ser Pro Thr His Arg Gly | | | |
| 260 | 265 | 270 | |
| Leu Tyr Ala Leu Ala Thr Tyr Arg Leu Tyr Ser Cys Tyr Ser Pro His | | | |
| 275 | 280 | 285 | |
| Glu Thr Tyr Arg Ala Arg Gly Gly Leu Thr His Arg Ala Ser Pro Leu | | | |
| 290 | 295 | 300 | |
| Glu Ala Leu Ala Ser Glu Arg Val Ala Leu Ile Leu Glu Thr Tyr Arg | | | |
| 305 | 310 | 315 | 320 |
| Val Ala Leu Thr Tyr Arg Val Ala Leu Gly Leu Asn Ala Ser Pro Thr | | | |
| 325 | 330 | 335 | |
| Tyr Arg Ala Arg Gly Ser Glu Arg Pro Arg Pro His Glu Ile Leu Glu | | | |
| 340 | 345 | 350 | |
| Ala Leu Ala Ser Glu Arg Val Ala Leu Ser Glu Arg Ala Ser Pro Gly | | | |
| 355 | 360 | 365 | |
| Leu Asn His Ile Ser Gly Leu Tyr Val Ala Leu Val Ala Leu Thr Tyr | | | |
| 370 | 375 | 380 | |
| Arg Ile Leu Glu Thr His Arg Gly Leu Ala Ser Asn Leu Tyr Ser Ala | | | |
| 385 | 390 | 395 | 400 |
| Ser Asn Leu Tyr Ser Thr His Arg Val Ala Leu Val Ala Leu Ile Leu | | | |
| 405 | 410 | 415 | |
| Glu Pro Arg Cys Tyr Ser Leu Glu Gly Leu Tyr Ser Glu Arg Ile Leu | | | |
| 420 | 425 | 430 | |
| Glu Ser Glu Arg Ala Ser Asn Leu Glu Ala Ser Asn Val Ala Leu Ser | | | |
| 435 | 440 | 445 | |
| Glu Arg Leu Glu Cys Tyr Ser Ala Leu Ala Ala Arg Gly Thr Tyr Arg | | | |
| 450 | 455 | 460 | |

Pro Arg Gly Leu Leu Tyr Ser Ala Arg Gly Pro His Glu Val Ala Leu
465 470 475 480

Pro Arg Ala Ser Pro Gly Leu Tyr Ala Ser Asn Ala Arg Gly Ile Leu
485 490 495

Glu Ser Glu Arg Thr Arg Pro Ala Ser Pro Ser Glu Arg Leu Tyr Ser
500 505 510

Leu Tyr Ser Gly Leu Tyr Pro His Glu Thr His Arg Ile Leu Glu Pro
515 520 525

Arg Ser Glu Arg Thr Tyr Arg Met Glu Thr Ile Leu Glu Ser Glu Arg
530 535 540

Thr Tyr Arg Ala Leu Ala Gly Leu Tyr Met Glu Thr Val Ala Leu Pro
545 550 555 560

His Glu Cys Tyr Ser Gly Leu Ala Leu Ala Leu Tyr Ser Ile Leu Glu
565 570 575

Ala Ser Asn Ala Ser Pro Gly Leu Ser Glu Arg Thr Tyr Arg Gly Leu
580 585 590

Asn Ser Glu Arg Ile Leu Glu Met Glu Thr Thr Tyr Arg Ile Leu Glu
595 600 605

Val Ala Leu Val Ala Leu Val Ala Leu Val Ala Leu Gly Leu Tyr Thr
610 615 620

Tyr Arg Ala Arg Gly Ile Leu Glu Thr Tyr Arg Ala Ser Pro Val Ala
625 630 635 640

Leu Val Ala Leu Leu Glu Ser Glu Arg Pro Arg Ser Glu Arg His Ile
645 650 655

Ser Gly Leu Tyr Ile Leu Glu Gly Leu Leu Glu Ser Glu Arg Val Ala
660 665 670